

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/738,404

Source: _____

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RAW SEQUENCE LISTING

DATE: 02/18/2005

PATENT APPLICATION: US/10/738,404

TIME: 11:13:47

Input Set : N:\Crf3\RULE60\10738404.raw.txt

Output Set: N:\CRF4\02182005\J738404.raw

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1 <110> APPLICANT: Philip E. Thorpe
2      Rolf A. Brekken
3 <120> TITLE OF INVENTION: ANTIBODY CONJUGATE METHODS FOR SELECTIVELY INHIBITING VEGF
4 <130> FILE REFERENCE: 4001.002585
5 <140> CURRENT APPLICATION NUMBER: US/10/738,404
6 <141> CURRENT FILING DATE: 2003-12-17
7 <150> PRIOR APPLICATION NUMBER: US/09/561,005
8 <151> PRIOR FILING DATE: 2000-04-28
9 <150> PRIOR APPLICATION NUMBER: 60/131,432
10 <151> PRIOR FILING DATE: 1999-04-28
11 <160> NUMBER OF SEQ ID NOS: 44
12 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 2149
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
18 <400> SEQUENCE: 1
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20      gctactatgc aataaatatc tcaagtttta acgaagaaaa acatcattgc agtgaaataa 120
21      aaaattttta aatttttagaa caaagctaac aaatggctag ttttctatga ttcttcttca 180
22      aacgctttct ttgaggggga aagagtcaaa caaacaagca gttttacctg aaataaagaa 240
23      ctagtttttag aggtcagaag aaaggagcaa gttttgcgag aggcacggaa ggagtgtgct 300
24      ggcagtacaa tgacagtttt cctttccttt gctttcctcg ctgccattct gactcacata 360
25      ggggtgcagca atcagcgccg aagtccagaa aacagtggga gaagatataa ccggattcaa 420
26      catgggcaat gtgcctacac tttcattctt ccagaacacg atggcaactg tcgtgagagt 480
27      acgacagacc agtacaacac aaacgctctg cagagagatg ctccacacgt ggaaccggat 540
28      ttctcttccc agaaacttca acatctggaa catgtgatgg aaaattatac tcagtggctg 600
29      caaaaacttg agaattacat tgtggaaaac atgaagtcgg agatggccca gatacagcag 660
30      aatgcagttc agaaccacac ggctaccatg ctggagatag gaaccagcct cctctctcag 720
31      actgcagagc agaccagaaa gctgacagat gttgagaccc aggtactaaa tcaaacttct 780
32      cgacttgaga tacagctgct ggagaattca ttatccacct acaagctaga gaagcaactt 840
33      cttcaacaga caaatgaaat cttgaagatc catgaaaaaa acagtttatt agaacataaa 900
34      atcttagaaa tggaaggaaa acacaaggaa gagttggaca ccttaaagga agagaaagag 960
35      aaccttcaag gcttggttac tcgtcaaaca tatataatcc aggagctgga aaagcaatta 1020
36      aacagagcta ccaccaacaa cagtgtcctt cagaagcagc aactggagct gatggacaca 1080
37      gtccacaacc ttgtcaatct ttgactaaa gaaggtggtt tactaaaggg aggaaaaaga 1140
38      gaggaagaga aaccatttag agactgtgca gatgtatatc aagctgggtt taataaaagt 1200
39      ggaatctaca ctatttatat taataatatg ccagaacca aaaaggtggt ttgcaatatg 1260
40      gatgtcaatg ggggaggttg gactgtaata caacatcgtg aagatggaag tctagatttc 1320
41      caaagaggct ggaaggaata taaaatgggt tttggaaatc cctccggtga atattggctg 1380
42      gggaatgagt ttatttttgc cattaccagt cagaggcagt acatgctaag aattgagtta 1440
43      atggactggg aagggaaccg agcctattca cagtatgaca gattccacat aggaaatgaa 1500
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46      aaatgtgccc tcatgttaac aggaggatgg tggtttgatg cttgtggccc ctccaatcta 1680
47      aatggaatgt tctatactgc gggacaaaac catggaaaac tgaatgggat aaagtggcac 1740
48      tacttcaaag ggcccagtta ctcttacgt tccacaacta tgatgattcg acctttagat 1800
49      ttttgaaagc gcaatgtcag aagcgattat gaaagcaaca aagaaatccg gagaagctgc 1860
50      caggtgagaa actgtttgaa aacttcagaa gcaaacaata ttgtctccct tccagcaata 1920
51      agtggtagtt atgtgaagtc accaaggttc ttgaccgtga atctggagcc gtttgagttc 1980
52      acaagagtct ctacttgggg tgacagtgtc cacgtggctc gactatagaa aactccactg 2040
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58 <212> TYPE: PRT
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64      20          25          30
65      Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
66      35          40          45
67      Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
68      50          55          60
69      Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
70      65          70          75          80
71      Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
72      85          90          95
73      Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
74      100         105         110
75      Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
76      115         120         125
77      Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
78      130         135         140
79      Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
80      145         150         155         160
81      Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
82      165         170         175
83      Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
84      180         185         190
85      Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
86      195         200         205
87      Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
88      210         215         220
89      Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
90      225         230         235         240
91      Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
92      245         250         255
93      Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
94      260         265         270

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98       290                     295                     300
99   Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
100      305                     310                     315                     320
101   Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
102                   325                     330                     335
103   Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
104                   340                     345                     350
105   Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
106       355                     360                     365
107   Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
108       370                     375                     380
109   Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
110      385                     390                     395                     400
111   Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
112                   405                     410                     415
113   Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
114                   420                     425                     430
115   Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
116       435                     440                     445
117   Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
118       450                     455                     460
119   Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
120      465                     470                     475                     480
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123   Asp Phe
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126 <211> LENGTH: 2269
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132   agcaggactg ttcttccac tgcaatctga cagtttactg catgcctgga gagaacacag 180
133   cagtaaaaac caggtttgct actggaaaaa gaggaaagag aagactttca ttgacggacc 240
134   cagccatggc agcgtagcag ccctgcgttt cagacggcag cagctcggga ctctggacgt 300
135   gtgtttgccc tcaagtttgc taagctgctg gtttattact gaagaaagaa tgtggcagat 360
136   tgttttcttt actctgagct gtgatcttgt cttggccgca gcctataaca actttcggaa 420
137   gagcatggac agcataggaa agaagcaata tcaggtccag catgggtcct gcagctacac 480
138   tttcctcctg ccagagatgg acaactgccg ctcttcctcc agcccctacg tgtccaatgc 540
139   tgtgcagagg gacgcgccgc tcgaatacga tgactcgggt cagaggctgc aagtgtctga 600
140   gaacatcatg gaaaacaaca ctcaagtggc aatgaagctt gagaattata tccaggacaa 660
141   catgaagaaa gaaatggtag agatacagca gaatgcagta cagaaccaga cggctgtgat 720
142   gatagaaata gggacaaacc tgttgaaaca aacagctgag caaacgcgga agttaactga 780
143   tgtggaagcc caagtattaa atcagaccac gagacttgaa cttcagctct tggaacactc 840
144   cctctcgaca aacaaattgg aaaaacagat tttggaccag accagtgaag taaacaaatt 900

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146 ccaactacag tcaataaaag aagagaaaga tcagctacag gtgttagtat ccaagcaaaa 1020
147 ttccatcatt gaagaactag aaaaaaaaaat agtgactgcc acggtgaata attcagttct 1080
148 tcaaaagcag caacatgatc tcatggagac agttaataac ttactgacta tgatgtccac 1140
149 atcaaaactca gctaaggacc ccactgttgc taaagaagaa caaatcagct tcagagactg 1200
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152 tattcagcga cgtgaggatg gcagcgttga ttttcagagg acttggaag aatataaagt 1380
153 gggatttggg aacccttcag gagaatattg gctgggaaat gagtttgttt cgcaactgac 1440
154 taatcagcaa cgctatgtgc ttaaaataca ccttaaagac tgggaaggga atgaggctta 1500
155 ctcatgtgat gaacatttct atctctcaag tgaagaactc aattatagga ttcaccttaa 1560
156 aggacttaca gggacagccg gcaaaataag cagcatcagc caaccaggaa atgattttag 1620
157 cacaaaggat ggagacaacg acaaatgtat ttgcaaatgt tcacaaatgc taacaggagg 1680
158 ctggtgggtt gatgcatgtg gtccttccaa cttgaacgga atgtactatc cacagaggga 1740
159 gaacacaaat aagttcaacg gcattaaatg gtactactgg aaaggctcag gctattcgct 1800
160 caaggccaca accatgatga tccgaccagc agatttctaa acatcccagt ccacctgagg 1860
161 aactgtctcg aactattttc aaagacttaa gccagtgca ctgaaagtca cggctgcgca 1920
162 ctgtgtcttc ttccaccaca gaggcggtgt gctcgggtgt gacgggaccc acatgctcca 1980
163 gattagagcc tgtaaacttt atcacttaaa cttgcatcac ttaacggacc aaagcaagac 2040
164 cctaaacatc cataattgtg attagacaga acacctatgc aaagatgaac ccgaggctga 2100
165 gaatcagact gacagtttac agacgtgtgt gtcacaacca agaattgtat gtgcaagttt 2160
166 atcagtaaat aactggaaaa cagaacactt atgttatata atacagatca tcttggaact 2220
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169 <210> SEQ ID NO: 4

170 <211> LENGTH: 496

171 <212> TYPE: PRT

172 <213> ORGANISM: Homo sapiens

173 <400> SEQUENCE: 4

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177 20 25 30
178 Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
179 35 40 45
180 Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
181 50 55 60
182 Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
183 65 70 75 80
184 Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
185 85 90 95
186 Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
187 100 105 110
188 Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
189 115 120 125
190 Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
191 130 135 140
192 Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
193 145 150 155 160
194 Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp

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195          165          170          175
196      Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
197          180          185          190
198      Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
199          195          200          205
200      Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
201          210          215          220
202      Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn
203      225          230          235          240
204      Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn
205          245          250          255
206      Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr
207          260          265          270
208      Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
209          275          280          285
210      Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn
211          290          295          300
212      Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly
213      305          310          315          320
214      Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln
215          325          330          335
216      Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu
217          340          345          350
218      Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg
219          355          360          365
220      Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr
221          370          375          380
222      Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg
223      385          390          395          400
224      Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile
225          405          410          415
226      Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys
227          420          425          430
228      Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp
229          435          440          445
230      Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln
231          450          455          460
232      Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser
233      465          470          475          480
234      Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe
235          485          490          495
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238 <211> LENGTH: 495
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 5
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/18/2005
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY

DATE: 02/18/2005

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Input Set : N:\Crf3\RULE60\10738404.raw.txt

Output Set: N:\CRF4\02182005\J738404.raw

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L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12